--The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically. A "primer" is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced (i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH). The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and intended use. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.--

A1

Please replace the paragraph beginning on page 19, line 3, with the following rewritten paragraph:

--Prokaryotic hosts may include *E. coli, S. typhirimurium, Serratia marcescens* and *Bacillus subtilis*. Eukaryotic hosts include yeasts such as *Pichia pastoris*, mammalian cells and insect cells.--

A2

Please replace the paragraph beginning on page 38, line 4, with the following rewritten paragraph:

--The sequences of the DNA fragments were assembled together by using a Seqman program (DNASTAR, Inc., Madison, WI) into a 23-kb seqment of DNA. There were 21 homologous *p28* genes in the DNA locus. The genes were designated as *p28-1* to *p28-21* according to their

A3

positions from the 5' end to the 3' end of the locus (Fig. 1). Most of the genes were tandemly arranged in one direction in the locus, and the last two genes (*p28-20* and *p28-21*) were in the complementary strand. The sizes of the genes ranged from 816 bp to 903 bp. The length of the non-coding sequences between the neighboring genes varied from 10 to 605-bp. The intergenic spaces between *p28-1* and *p28-2* and between *p28-6* and *p28-7* encoded a 150 amino acid protein and a 195 amino acid protein, respectively, and the two proteins had no sequence similarity to any known proteins.--

Please delete the paragraph beginning on page 42, line 19 (Example 13).

Please replace the paragraph beginning on page 44, line 14, with the following rewritten paragraph:

--Sequencing of the *p28* multigene locus in the *E. chaffeensis* in this study will contribute to the investigation of the origin of the multigene family and the function of the multigenes. Gene families are thought to have arisen by duplication of an original ancestral gene, with different members of the family then diverging as a consequence of mutations during evolution. The most conserved *p28* gene among the species of *Ehrlichia* should be the ancestral gene. *E. chaffeensis p28-15* to *p28-19* are the most similar genes to the *p28* of *E. canis* and *E. muris*. Therefore, the *p28* genes might have arisen from one of the *p28-15* to *p28-19* genes. The wide presence of the *p28/msp-2* multigenes in the *Ehrlichia, Anaplasma,* and *Cowdria* indicate that these organisms are phylogenetically related. The significant sequence identity between the *p28* multigene family and the *msp-2* multigene family indicates that the two gene families orginated from a common ancestor gene.--

A4